

1 MetTyrlleTyrlleValAlaLeuValGlyPheLeuAlaasnPro 20
6995 ATGATATTACCTACCTTTTTCCTTTGCTTACCTTGGCGGTTTTTACTTGCATAATCAAAATCCA 6936
21 llaasnAlaaspLeuArgGlylleValGlySerProPheLeuAlaSerGlylleSerAsn 40
6935 ATCAATCGCGATTTACGAAAAATTGTTGGCTCACCATTTTACGCTCTCGAATTTCCAAC 6876
41 pheValGlySerllePheLeuGlyllelleThrLeuValThrSerGlnThrLeuPhePro 60
6875 TTGTTGCTTCGATTTTTCAGCAATCATCATTACTGACAACTCAAAACACTTTTTCCT 6816
61 SerPheGlnPheValGlySerHisProValTrpIleTrpIleGlyGlyValLeuGlyGly 80
6815 ACTTTTCAATTTGTTGCTTCACACCCAGCATGCAATGCAATGCGGTTCTTGGTGCG 6756
81 llePheLeuThrSerAsnValLeuPheProArgLeuGlyAlaValGlnThrVallle 100
6755 ATTTTCCTAACGCTCATAGCTTTTACTTTTTCAGAGATAGCAGCTGTCCAAACAGCATT 6696
101 LeuProilleLeuGlyArgilleLeuMetGlyThrLeuilleAspSerPheGlyTrpPheHis 120
6695 TTACCTATTTTGGCGTCAAAATATGATGGCGACACTTATTCATTTCATTGGCTGCTTCAT 6636
121 AlaMetGlnLeuProMetThrLeuMetArgPheLeuGlyValillelleThrLeuAlaGly 140
6635 GCCATCGAACTTCGATCTCTGATCGCGCTTTTTCGCGAATATCATTTACTTTAGCTGCT 6576
141 ValilleValilleValleuProAsnLeuGlyGlyGlnAlaGlnThrHisGlnThr 160
6575 GTTATTGTCGCGGTTGTTCTTCCTAATTTTAAAGCAAAACAGCAACGACCAACT 6516
161 AsnLeuLeuGlyTrpArgilleTrpAlaValilleValGlyAlaMetSerAlaAlaGlnGln 180
6515 AACTTACTAGCGTCGCCGATATGCGCGGCTCATCGTTGCCCAATGTCAGCTGCTCAACA 6456
181 AlaIleAsnGlyArgLeuGlyValleuLeuGlnAsnThrAlaGlnAlaThrPheValSer 200
6455 CCAATTAATGCGCCGATTTGCGAGTTTACTTGAAATACTGCACAAACGACGCTTTTCTTCG 6396
201 PhePheilleGlyPheLeuAlaIlePheilleValSerLeuPheilleAspArgLeuPro 220
6395 TTCTTCATTGCAATTTTACGCTATTTTTCGTTCTCTCTTTTATTGACCAACGCTTTGCCA 6336
221 LysilleSerGlnLeuGlyLysAlaLysProTrpAsnGlylleGlyGlyPheLeuGlyAla 240
6335 AAAATTCAGCAATTAAGAAAAAGCAAAACCTTGCAATGCAATTGCTGCATTTTTCAGCAGCT 6276
241 SerilleValPheAlaThrValAlaValProGlnilleGlyAlaGlyLeuThrIleMet 260
6275 TCATTTCGTTTTTCGAACAGCTGCTTGGTTCCTCCGCAAAATTCGTCAGCGCTCACAATATATC 6216
261 MetGlyLeuIleGlyGlnilleLeuGlySerMetLeuValGlnGlnPheGlyTrpTrpArg 280
6215 ATGCGCTTCATTTCGACCAAAATTTAGCGCAGTATGTTGCTTCAACAAATTTGCTTGGCGCG 6156
281 SerSerLysTrpGlyIleGlnIleTrpGlnIleValGlylleLeuIleMetLeuThrGly 300
6155 TCAGTAATAATATGCGCATTCAAATTTGCGAAATTCGTCGATTTCTAATATATCTGACCGCA 6096
301 llellePheilleLysPheLeu 307
6095 ATAAATTCATTAATTTTIA 6075

RESULT :

AB55104
ID AB55104 standard: protein: 307 AA.

AC AB55104;

DT 29-AUG-2003 (revised)

DT 16-MAY-2002 (first entry)

DE Lactococcus lactis protein y8b.

KD Biosource; Biodegradation; Lactic bacterium; yogurt; cheese.

OS Lactococcus lactis; IL1403.

PN F8607448-AL

PD 12-OCT-2001

PF 11-APR-2000; 2000FB-00004630.

PR 11-APR-2000; 2000FB-00004630.

RA (INRA) INRA INST NAT RECH AGRONOMIQUE.

PI Bolotine A, Sorokine A, Henault P, Ehrlich SD;

DB MPI; 2002-043416/06.

PT New nucleotide sequence useful in the identification of Lactococcus lactis and related species.

PS Claim 6; SEQ ID NO 1006; 2504pp; French.

CC The present invention is related to a Lactococcus lactis nucleotide

CC sequence (AB550521) and related proteins (AB552300-AB555621). The nucleic

CC acid sequence is useful in the detection and/or amplification of nucleic

CC acid sequence, particularly to identify Lactococcus lactis or related

CC species. The proteins of the invention are useful for the biotechnologies or

CC biodegradation of a composition of interest. The invention helps research

CC in lactic bacteria, particularly useful in the production of yogurt and

CC cheese. Note: The sequence data for this patent is based on equivalent

CC patent WO200177334 (published 10-OCT-2001) which is available in

CC electronic format directly from WIPO at

CC http://www.int/pat/publications_sequences. (Updated on 29-AUG-2003 to

CC standardize OS field)

SQ Sequence 307 AA;

Query Match
Best Local Similarity 98.04; Pred. No. 9,4e-161;
98.54; Score 1529; DB 5; Length 307;
Matches 301; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVAIALATVCCGFLTANQMPIMATLPMKIVGCSPTLASGIZSMVCSISFLCIITLVTSQTLFP 60
DB 1 MVAIALATVCCGFLTANQMPIMATLPMKIVGCSPTLASGIZSMVCSISFLCIITLVTSQTLFP 60

QY 61 SFQVCSHPVQIWCICGFLITSMVLLTPPLCAVQGVLPILCGIIMGTLIDISGLATH 120
DB 61 SFQVCSHPVQIWCICGFLITSMVLLTPPLCAVQGVLPILCGIIMGTLIDISGLATH 120

QY 121 AMQPMTHMRLGCVIITLACVAVAPMLPMKMKKATETHQMTLCAHIAVAVGAM3AAQ 180
DB 121 AMQPMTHMRLGCVIITLACVAVAPMLPMKMKKATETHQMTLCAHIAVAVGAM3AAQ 180

QY 191 AINCHLGVLTENITAGATVVSITIFLAIIFIVSITIDRRALPKI3ELXKAKPMGICGLCA 240
DB 191 AINCHLGVLTENITAGATVVSITIFLAIIFIVSITIDRRALPKI3ELXKAKPMGICGLCA 240

QY 241 SIVFATVAVAPQICAGLTIMGELICQILCSMLVQGCAGM33KXK6IQIWQIVGILIMLTG 300
DB 241 SIVFATVAVAPQICAGLTIMGELICQILCSMLVQGCAGM33KXK6IQIWQIVGILIMLTG 300

QY 301 IIFIKLT 307
DB 301 IIFIKLT 307